

WO 2005/049655

1/12

SEQUENCE LISTING

<110> Klinikum der Universitaet Muenchen Grosshadern-Innenstadt
<120> Leptin antagonist and method for the quantitative measurement of leptin
<130> LM01P002WO
<150> DE 103 53 953.4
<151> 2003-11-17
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<170> PatentIn version 3.1
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Lys Phe Met Ser Thr Ser Ile Gly Asp Arg Val Asn Ile Thr Cys Lys
35 40 45

Ala Thr Gln Asn Val Arg Thr Ala Val Thr Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Ser Pro Gln Ala Leu Ile Phe Leu Ala Ser Asn Arg His Thr
65 70 75 80

Gly Val Pro Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Thr Ile Asn Asn Val Lys Ser Glu Asp Leu Ala Asp Tyr Phe Cys
100 105 110

Leu Gln His Trp Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
 180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
 195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
 210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys Xaa Xaa
 225 230 235 240

Ser Arg Val Lys Arg Xaa Gln Ser Xaa Gly Gly Pro Gly Thr Pro Ile
 245 250 255

Arg Pro Ile Gly Xaa Pro Tyr Tyr Asn Ser Leu Gly Gly Phe Gln
 260 265 270

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tta ctc gct gcc caa cca gcc atg gcc gag ctc gtg atg acc cag tct 95
 Leu Leu Ala Ala Gln Pro Ala Met Ala Glu Leu Val Met Thr Gln Ser
 20 25 30

cca aaa ttc atg tcc aca tca ata gga gac agg gtc aat atc acc tgc 143
 Pro Lys Phe Met Ser Thr Ser Ile Gly Asp Arg Val Asn Ile Thr Cys
 35 40 45

aag gcc act cag aat gtt cgt act gct gtt acc tgg tat caa cag aaa Lys Ala Thr Gln Asn Val Arg Thr Ala Val Thr Trp Tyr Gln Gln Lys 50 55 60	191
cca ggg cag tct cct caa gca ctg att ttc ttg gca tcc aac cgg cac Pro Gly Gln Ser Pro Gln Ala Leu Ile Phe Leu Ala Ser Asn Arg His 65 70 75	239
act ggt gtc cct gct cga ttc aca ggc agt gga tct ggg aca gat ttc Thr Gly Val Pro Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe 80 85 90 95	287
act ctc acc att aac aat gtg aaa tct gaa gac ctg gca gat tat ttc Thr Leu Thr Ile Asn Asn Val Lys Ser Glu Asp Leu Ala Asp Tyr Phe 100 105 110	335
tgt cta caa cat tgg aat tat cct ctc acg ttc ggc tcg ggg aca aag Cys Leu Gln His Trp Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys 115 120 125	383
ttg gaa ata aaa cgg gct gat gct gca cca act gta tcc atc ttc cca Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro 130 135 140	431
cca tcc agt gag cag tta aca tct gga ggt gcc tca gtc gtg tgc ttc Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe 145 150 155	479
ttg aac aac ttc tac ccc aaa gac atc aat gtc aag tgg aag att gat Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp 160 165 170 175	527
ggc agt gaa cga caa aat ggc gtc ctg aac agt tgg act gat cag gac Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp 180 185 190	575
agc aaa gac agc acc tac agc atg agc agc acc ctc acg ttg acc aag Ser Lys Asp Ser Thr Tyr Ser Met Ser Thr Leu Thr Leu Thr Lys 195 200 205	623
gac gag tat gaa cga cat aac agc tat acc tct gag gcc act cac aag Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys 210 215 220	671
aca tca act tca ccc att gtc aag agc ttc aac agg gga gag tgg tag Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235	719
taa tct aga gtt aag cgg ccg caa tcg agg ggg ggc ccg gta ccc caa Ser Arg Val Lys Arg Pro Gln Ser Arg Gly Gly Pro Val Pro Gln 240 245 250	767
ttc gcc cta tag ggg ngc cgt att aca att cac tgg gcg gcg gtt ttc Phe Ala Leu Gly Xaa Arg Ile Thr Ile His Trp Ala Ala Val Phe 255 260 265	815
aan Xaa	818

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20 25 30

Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu Ser
35 40 45

Gly Pro Gly Leu Val Ala Pro Ser Glu Ser Leu Ser Ile Thr Cys Thr
50 55 60

Ile Ser Gly Phe Ser Leu Thr Asp Asp Gly Val Ser Trp Ile Arg Gln
65 70 75 80

Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Gly
85 90 95

Ser Thr Tyr Phe Asn Ser Leu Phe Lys Ser Arg Leu Ser Ile Thr Arg
100 105 110

Asp Asn Ser Lys Ser Gln Val Phe Leu Glu Met Asp Ser Leu Gln Thr
115 120 125

Asp Asp Thr Ala Met Tyr Tyr Cys Ala Lys His Asp Gly His Glu Thr
130 135 140

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Lys
145 150 155 160

Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
165 170 175

Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
180 185 190

Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
195 200 205

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His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
 210 215 220

Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
 225 230 235 240

Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
 245 250 255

Pro Arg Asp Cys Thr Ser His His His His His Xaa Ala Ser Leu
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Val Val Ala Val Ala Leu His Ser Phe Val Xaa Ile Lys Ala Asn Arg
 275 280 285

Arg Pro Ala Xaa
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gtc ata atg aaa tac ctt ttn gcc tac ggg cca gcc gct gga ttg tta 96
 Val Ile Met Lys Tyr Leu Xaa Ala Tyr Gly Pro Ala Ala Gly Leu Leu
 20 25 30

tta ctc gct gcc caa cca gcc atg gcc cag gtg aaa ctg ctc gag tca 144
 Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu Ser
 35 40 45

gga cct ggc ctg gtg gcg ccc tca gag agc ctg tcc atc aca tgc act 192
 Gly Pro Gly Leu Val Ala Pro Ser Glu Ser Leu Ser Ile Thr Cys Thr
 50 55 60

atc tca ggg ttc tca tta acc gac gat ggt gta agc tgg att cgg cag 240
 Ile Ser Gly Phe Ser Leu Thr Asp Asp Gly Val Ser Trp Ile Arg Gln
 65 70 75 80

cct cca gga aag ggt ctg gag tgg ctg gga gta ata tgg ggt gga 288

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Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Gly	Gly	
					85				90				95			
agc	aca	tac	ttt	aat	tca	ctt	ttc	aaa	tcc	aga	ctg	agc	atc	acc	agg	336
Ser	Thr	Tyr	Phe	Asn	Ser	Leu	Phe	Lys	Ser	Arg	Leu	Ser	Ile	Thr	Arg	
					100				105				110			
gac	aac	tct	aag	agc	caa	gtt	ttc	tta	gaa	atg	gac	agt	cta	caa	act	384
Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Glu	Met	Asp	Ser	Leu	Gln	Thr	
					115				120				125			
gat	gac	aca	gcc	atg	tac	tac	tgc	gcc	aaa	cat	gac	gga	cac	gag	act	432
Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Lys	His	Asp	Gly	His	Glu	Thr	
					130				135				140			
atg	gac	tat	tgg	ggt	caa	gga	acc	tca	gtc	acc	gtc	tcc	tca	tcc	aaa	480
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ser	Lys	
					145				150				155			160
acg	aca	ccc	cca	tct	gtc	tat	cca	ctg	gcc	cct	gga	tct	gct	gcc	caa	528
Thr	Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	
					165				170				175			
act	aac	tcc	atg	gtg	acc	ctg	gga	tgc	ctg	gtc	aag	ggc	tat	ttc	cct	576
Thr	Asn	Ser	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	
					180				185				190			
gag	cca	gtg	aca	gtg	acc	tgg	aac	tct	gga	tcc	ctg	tcc	agc	ggt	gtg	624
Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	
					195				200				205			
cac	acc	ttc	cca	gct	gtc	ctg	cag	tct	gac	ctc	tac	act	ctg	agc	agc	672
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	
					210				215				220			
tca	gtg	act	gtc	ccc	tcc	agc	acc	tgg	ccc	agc	gag	acc	gtc	acc	tgc	720
Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	
					225				230				235			240
aac	gtt	gcc	cac	ccg	gcc	agc	agc	acc	aag	gtg	gac	aag	aaa	att	gtg	768
Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	
					245				250				255			
ccc	agg	gat	tgt	act	agt	cat	cat	cat	cat	cat	cat	taa	gct	agc	cta	816
Pro	Arg	Asp	Cys	Thr	Ser	His	Ala	Ser	Leu							
					260				265				270			
gtg	gtg	gct	gtg	gct	ctc	cat	tcg	ttt	gtg	ang	ata	aag	gcc	aat	cgn	864
Val	Val	Ala	Ala	Leu	His	Ser	Phe	Val	Xaa	Ile	Lys	Ala	Asn	Arg		
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aga	cct	gcn	cna													876
Arg	Pro	Ala	Xaa													
			290													

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cag	gag	tca	gga	act	gaa	gtg	gta	aag	cct	ggg	gct	tca	gtg	aag	ttg	103
Gln	Glu	Ser	Gly	Thr	Glu	Val	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Leu	
10					15								20			

tcc	tgc	aag	gct	tct	ggc	tac	atc	ttc	aca	agt	tat	gat	ata	gac	tgg	151
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Thr	Ser	Tyr	Asp	Ile	Asp	Trp	
25					30						35					

gtg	agg	cag	acg	cct	gaa	cag	gga	ctt	gag	tgg	att	gga	tgg	att	ttt	199
Val	Arg	Gln	Thr	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Trp	Ile	Phe	
40					45						50					

cct	gga	gag	ggg	agt	act	gaa	tac	aat	gag	aag	ttc	aag	ggc	agg	gcc	247
Pro	Gly	Glu	Gly	Ser	Thr	Glu	Tyr	Asn	Glu	Lys	Phe	Lys	Gly	Arg	Ala	
55					60					65			70			

aca	ctg	agt	gta	gac	aag	tcc	agc	aca	gcc	tat	atg	gag	ctc	act	295
Thr	Leu	Ser	Val	Asp	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Thr	
75					80						85				

agg	ctg	aca	tct	gag	gac	tct	gct	tat	ttc	tgt	gct	aga	ggg	gac	343
Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Gly	Asp
90					95						100				

tac	tat	agg	cgc	tac	ttt	gac	ttg	tgg	ggc	caa	ggg	acc	acg	gtc	acc	391
Tyr	Tyr	Arg	Arg	Tyr	Phe	Asp	Leu	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	
105					110					115						

gtc	tcc	tca	tgt	gga	ggc	ggt	tca	ggc	gga	ggt	ggc	tct	ggc	ggt	ggc	439
Val	Ser	Ser	Cys	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
120			125							130						

gga	tct	gac	att	gag	ctc	acc	cag	tct	cca	gca	atc	atg	tct	gca	tct	487
Gly	Ser	Asp	Ile	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	
135			140						145			150				

cca	ggg	gag	agg	gtc	acc	atg	acc	tgc	agt	gcc	agc	tca	agt	ata	cgt	535
Pro	Gly	Glu	Arg	Val	Thr	Met	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Ile	Arg	
155					160						165					

tac	ata	tat	tgg	tac	caa	cag	aag	cct	gga	tcc	tcc	ccc	aga	ctc	ctg	583
Tyr	Ile	Tyr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Arg	Leu	Leu	
170			175								180					

att	tat	gac	aca	tcc	aac	gtg	gct	cct	gga	gtc	cct	ttt	cgc	ttc	agt	631
Ile	Tyr	Asp	Thr	Ser	Asn	Val	Ala	Pro	Gly	Val	Pro	Phe	Arg	Phe	Ser	
185					190						195					

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ggc	agt	ggg	tct	ggg	acc	tct	tat	tct	ctc	aca	atc	aac	cga	atg	gag	679
Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Asn	Arg	Met	Glu	
200					205				210							
gct	gag	gat	gct	gcc	act	tat	tac	tgc	cag	gag	tgg	agt	ggt	tat	cct	727
Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Glu	Trp	Ser	Gly	Tyr	Pro	
215					220				225			230				
ctc	acg	ttc	ggc	tcg	ggc	acc	aag	cg	gaa	atc	aaa	cg	gc	gc	gca	775
Leu	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Arg	Glu	Ile	Lys	Arg	Ala	Ala	Ala	
235							240			245						
ggt	g	cg	gt	cc	tat	cc	gat	cc	ct	gaa	cc	cg	ct	g	ccgcata	824
Gly	Ala	Pro	Val	Pro	Tyr	Pro	Asp	Pro	Leu	Glu	Pro	Pro	Arg			
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				20				25				30			

Ser	Tyr	Asp	Ile	Asp	Trp	Val	Arg	Gln	Thr	Pro	Glu	Gln	Gly	Leu	Glu
					35		40		45						

Trp	Ile	Gly	Trp	Ile	Phe	Pro	Gly	Glu	Gly	Ser	Thr	Glu	Tyr	Asn	Glu
					50		55		60						

Lys	Phe	Lys	Gly	Arg	Ala	Thr	Leu	Ser	Val	Asp	Lys	Ser	Ser	Ser	Thr
65							70		75			80			

Ala	Tyr	Met	Glu	Leu	Thr	Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr
					85			90			95				

Phe	Cys	Ala	Arg	Gly	Asp	Tyr	Tyr	Arg	Arg	Tyr	Phe	Asp	Leu	Trp	Gly
					100		105		110						

Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Cys	Gly	Gly	Ser	Gly	Gly	
							115		120		125				

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Gly Gly Ser Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro
 130 135 140

Ala Ile Met Ser Ala Ser Pro Gly Glu Arg Val Thr Met Thr Cys Ser
 145 150 155 160

Ala Ser Ser Ser Ile Arg Tyr Ile Tyr Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

Ser Ser Pro Arg Leu Leu Ile Tyr Asp Thr Ser Asn Val Ala Pro Gly
 180 185 190

Val Pro Phe Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 195 200 205

Thr Ile Asn Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 210 215 220

Glu Trp Ser Gly Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Arg Glu
 225 230 235 240

Ile Lys Arg Ala Ala Ala Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu
 245 250 255

Glu Pro Arg

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actctaagag ccaagtttc ttagaaatgg acagtctaca aactgatgac acagccatgt	300	
actactgcgc caaacatgac ggacacgaga ctatggacta ttggggtcaa ggaacctcag	360	
tcaccgtctc ctcatccaaa acgacacccc catctgtcta tccactggcc cctggatctg	420	
ctgccccaaac taactccatg gtgaccctgg gatgcctggt caagggttat ttccctgagc	480	

cagtgacagt gacctggaac tctggatccc tgtccagcgg tgtgcacacc ttcccagctg	540
tcctgcagtc tgacctctac actctgagca gctcagtgac tgtccctcc agcacctggc	600
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aaattgtgcc cagggattgt actagtggtg gcggaggtag tggtggcgga gtagcggtg	720
gcggaggttc tggtggcgga ggttccgaat tcctcgaggt gcccatccaa aaagtccaag	780
atgacaccaa aaccctcatc aagacaattg tcaccaggat caatgacatt tcacacacgc	840
agtcaagtctc ctccaaacag aaagtacccg gtttggactt cattcctggg ctccacccca	900
tcctgacctt atccaagatg gaccagacac tggcagtcta ccaacagatc ctcaccagta	960
tgccttccag aaacgtgatc caaatatcca acgacctgga gaacctccgg gatcttcttc	1020
acgtgctggc cttctctaag agctgccact tgccctggc cagtggcctg gagaccttgg	1080
acagcctggg gggtgtcctg gaagcttcag gctactccac agaggtggtg gccctgagca	1140
ggctgcaggg gtctctgcag gacatgctgt ggcagctgga cctcagccct gggtgcacta	1200
gtcatcatca tcatcatcat taagctagcc tagtggtggc ggtggctctc ca	1252

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30			

Asp Asp Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu			
35	40	45	
45			

Trp Leu Gly Val Ile Trp Gly Gly Ser Thr Tyr Phe Asn Ser Leu			
50	55	60	
60			

Phe Lys Ser Arg Leu Ser Ile Thr Arg Asp Asn Ser Lys Ser Gln Val			
65	70	75	80
75	80		

Phe Leu Glu Met Asp Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr			
85	90	95	
95			

Cys Ala Lys His Asp Gly His Glu Thr Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ser Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Thr Ser Gly
210 215 220

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser Glu Phe Leu Glu Val Pro Ile Gln Lys Val Gln Asp Asp
245 250 255

Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser
260 265 270

His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe
275 280 285

Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr
290 295 300

Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val
305 310 315 320

Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val
325 330 335

Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu

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340

345

350

Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr
355 360 365

Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu
370 375 380

Trp Gln Leu Asp Leu Ser Pro Gly Cys Thr Ser His His His His His
385 390 395 400

His